

BC #4

PCT09

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/719,088A

DATE: 08/01/2001
 TIME: 14:21:53

Input Set : A:\92979.txt
 Output Set: N:\CRF3\08012001\I719088A.raw

4 <110> APPLICANT: Garvan Institute of Medical Research
 6 <120> TITLE OF INVENTION: NPY-Y7 Receptor Gene
 W--> 0 <130> FILE REFERENCE:
 C--> 8 <140> CURRENT APPLICATION NUMBER: US/09/719,088A
 C--> 9 <141> CURRENT FILING DATE: 2001-05-09
 11 <150> PRIOR APPLICATION NUMBER: PP 4385
 12 <151> PRIOR FILING DATE: 1998-06-29
 14 <160> NUMBER OF SEQ ID NOS: 5
 16 <170> SOFTWARE: PatentIn Ver. 2.1
 18 <210> SEQ ID NO: 1
 19 <211> LENGTH: 14
 20 <212> TYPE: PRT
 21 <213> ORGANISM: Artificial Sequence
 23 <220> FEATURE:
 24 <223> OTHER INFORMATION: Description of Artificial Sequence: N-terminal
 consensus sequence
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 W--> 28 <221> NAME/KEY: misc-feature
 29 <222> LOCATION: (2)..(3)..(5)..(10)
 30 <223> OTHER INFORMATION: Xaa = any codable amino acid
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 34 1 5 10
 37 <210> SEQ ID NO: 2
 38 <211> LENGTH: 408
 39 <212> TYPE: PRT
 40 <213> ORGANISM: Homo sapiens
 42 <400> SEQUENCE: 2
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 44 1 5 10 15
 46 His Pro Ile Trp Asn Val Asn Asp Thr Lys His His Leu Tyr Ser Asp
 47 20 25 30
 49 Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala
 50 35 40 45
 52 Ala Ile Phe Ile Ile Ser Tyr Phe Leu Ile Phe Phe Leu Cys Met Met
 53 50 55 60
 55 Gly Asn Thr Val Val Cys Phe Ile Val Met Arg Asn Lys His Met His
 56 65 70 75 80
 58 Thr Val Thr Asn Leu Phe Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu
 59 85 90 95
 61 Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala
 62 100 105 110
 64 Gly Trp Pro Phe Gly Asn Thr Met Cys Lys Ile Ser Gly Leu Val Gln
 65 115 120 125
 67 Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val
 68 130 135 140
 70 Asp Arg Phe Gln Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Ile

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71	145	150	155	160
73	Lys Thr Ala Phe Val Ile Ile Met Ile Ile Trp Val Leu Ala Ile Thr			
74	165	170	175	
76	Ile Met Ser Pro Ser Ala Val Met Leu His Val Gln Glu Glu Lys Tyr			
77	180	185	190	
79	Tyr Arg Val Arg Leu Asn Ser Gln Asn Lys Thr Ser Pro Val Tyr Trp			
80	195	200	205	
82	Cys Arg Glu Asp Trp Pro Asn Gln Glu Met Arg Lys Ile Tyr Thr Thr			
83	210	215	220	
85	Val Leu Phe Ala Asn Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile			
86	225	230	235	240
88	Met Tyr Gly Arg Ile Gly Ile Ser Leu Phe Arg Ala Ala Val Pro His			
89	245	250	255	
91	Thr Gly Arg Lys Asn Gln Glu Gln Trp His Val Val Ser Arg Lys Lys			
92	260	265	270	
94	Gln Lys Ile Ile Lys Met Leu Leu Ile Val Ala Leu Leu Phe Ile Leu			
95	275	280	285	
97	Ser Trp Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Ala Asp			
98	290	295	300	
100	Leu Ser Pro Asn Glu Leu Gln Ile Ile Asn Ile Tyr Ile Tyr Pro Phe			
101	305	310	315	320
103	Ala His Trp Leu Ala Phe Gly Asn Ser Ser Val Asn Pro Ile Ile Tyr			
104	325	330	335	
106	Gly Phe Phe Asn Glu Asn Phe Arg Arg Gly Phe Gln Glu Ala Phe Gln			
107	340	345	350	
109	Leu Gln Leu Cys Gln Lys Arg Ala Lys Pro Met Glu Ala Tyr Thr Leu			
110	355	360	365	
112	Lys Ala Lys Ser His Val Leu Ile Asn Thr Ser Asn Gln Leu Val Gln			
113	370	375	380	
115	Glu Ser Thr Phe Gln Asn Pro His Gly Glu Thr Leu Leu Tyr Arg Lys			
116	385	390	395	400
118	Ser Ala Glu Asn Pro Asn Arg Asn			
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123	<211> LENGTH: 405			
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131	Asn His Ile Trp Ser Gly Asn Asp Thr Gln His His Trp Tyr Ser Asp			
132	20	25	30	
134	Ile Asn Ile Thr Tyr Val Asn Tyr Tyr Leu His Gln Pro Gln Val Ala			
135	35	40	45	
137	Ala Val Phe Ile Ser Ser Tyr Leu Leu Ile Phe Val Leu Cys Met Val			
138	50	55	60	
140	Gly Asn Thr Val Val Cys Phe Ile Val Ile Arg Asn Arg His Met His			
141	65	70	75	80
143	Thr Val Thr Asn Phe Leu Ile Leu Asn Leu Ala Ile Ser Asp Leu Leu			

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144	85	90	95
146	Val Gly Ile Phe Cys Met Pro Ile Thr Leu Leu Asp Asn Ile Ile Ala		
147	100	105	110
149	Gly Trp Pro Phe Gly Ser Ser Met Cys Lys Ile Ser Gly Leu Val Gln		
150	115	120	125
152	Gly Ile Ser Val Ala Ala Ser Val Phe Thr Leu Val Ala Ile Ala Val		
153	130	135	140
155	Asp Arg Phe Arg Cys Val Val Tyr Pro Phe Lys Pro Lys Leu Thr Val		
156	145	150	155
158	160	Lys Thr Ala Phe Val Thr Ile Val Ile Ile Trp Gly Leu Ala Ile Ala	
159	165	170	175
161	Ile Met Thr Pro Ser Ala Ile Met Leu His Val Gln Glu Glu Lys Tyr		
162	180	185	190
164	Tyr Arg Val Arg Leu Ser Ser His Asn Lys Thr Ser Thr Val Tyr Trp		
165	195	200	205
167	Cys Arg Glu Asp Trp Pro Arg His Glu Met Arg Arg Ile Tyr Thr Thr		
168	210	215	220
170	225	230	235
171	240	Leu Phe Ala Ile Ile Tyr Leu Ala Pro Leu Ser Leu Ile Val Ile	
173	Met Tyr Ala Arg Ile Gly Ala Ser Leu Phe Lys Thr Ala Ala His Cys		
174	245	250	255
176	Thr Gly Lys Gln Arg Pro Val Gln Cys Met Tyr Gln Glu Lys Gln Lys		
177	260	265	270
179	270	275	280
180	285	290	295
182	Leu Pro Leu Trp Thr Leu Met Met Leu Ser Asp Tyr Thr Asp Leu Ser		
183	300	305	310
185	320	Pro Asn Lys Leu Arg Ile Ile Asn Ile Tyr Ile Tyr Pro Phe Ala His	
186	325	330	335
188	340	Trp Leu Ala Phe Cys Asn Ser Ser Val Asn Pro Ile Ile Tyr Gly Phe	
189	345	350	355
191	360	Phe Asn Glu Asn Phe Arg Asn Gly Phe Gln Asp Ala Phe Gln Ile Cys	
192	365	370	375
194	380	Gln Lys Lys Ala Lys Pro Gln Glu Ala Tyr Ser Leu Arg Ala Lys Arg	
195	385	390	395
197	400	Asn Ile Val Ile Asn Thr Ser Gly Leu Leu Val Gln Glu Pro Val Ser	
198	405	410	415
200	420	Gln Asn Pro Gly Gly Glu Asn Leu Gly Cys Gly Lys Ser Ala Asp Asn	
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208	<211> LENGTH: 1903		
209	<212> TYPE: DNA		
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214	cacgcctggc taattttttt gtatTTTtag tagggacggc gtttcactgt gtttagccaga 120		
215	tggtctccat ctccccacct cgtgatccac ccacccggc ctcccaaagt gctgggatta 180		

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216 caggcgtgag accgcgcccc gccaatttcc tttcttagtt gcctctgcc acctcttc 240
 217 ttctgcttcc atattacagg tttcctcagt tgcaaatta ggtatgttaat tatagtttt 300
 218 gacataacaag aaacatcaaa aagattgaat gtctaataa gagtgaagca tgttagatcg 360
 219 tgactgctat gttcatcatg aatgagaat gggacacaaa ctttcagaa aactggcatc 420
 220 ccatctggaa tgtcaatgac acaaaggcatc atctgtactc agatattaat attacctatg 480
 221 tgaactacta tcttcaccag cctcaagtgg cagcaatctt cattatttcc tactttctga 540
 222 tcttcctttt gtgcgtatg gaaatactg tggttgtt tattgtatg aggaacaaac 600
 223 atatgcacac agtcaactat ctcttcatct taaacctggc cataagtgtat ttactagttg 660
 224 gcatattctg catgcctata acactgctgg acaatattat agcaggatgg ccatttgaa 720
 225 acacgtgtg caagatcagt ggattggtcc agggaatatc tgtcgcagct tcagtctta 780
 226 cgtagttgc aattgtgtt gataggttcc agtgtgtgtt ctacccttt aaaccaaagc 840
 227 tcaactatcaa gacagcggtt gtcattattt tgatcatctg ggtcctagcc atcaccatta 900
 228 tgtctccatc tgcagtaatg ttacatgtgc aagaagaaaa atattaccga gtgagactca 960
 229 actcccagaa taaaaccagt ccagtctact ggtgccgggaa agactggcca aatcaggaaa 1020
 230 tgaggaagat ctacaccact gtgctgtttt ccaacatcta cctggctccc ctctccctca 1080
 231 ttgtcatcat gtatggaagg attggaattt cactttcag ggctgcagtt cctcacacag 1140
 232 gcaggaagaa ccaggagcag tggcacgtgg tgtccaggaa gaagcagaag atcattaaga 1200
 233 tgctcctgtat tgtggccctg ctttttattt tctcatggct gcccctgtgg actctaata 1260
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 238 catctaataca gcttgcacg gaatctacat ttcaaaaccc tcatgggaa accttgctt 1560
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 241 tatttaaatc cattgtttt tgtggcttgc cacttcaat ttttcaaaaatg atgttctaaa 1740
 242 taaaacattt actgaaagcc ctctctggca aaaaaattaa aaataaacaat aaatggtcat 1800
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 247 <211> LENGTH: 1228
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 249 <213> ORGANISM: Mus musculus
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 254 tatctccacc agccccaaatg ggcagctgtc ttcatcagct cttacactt gatctttgtc 180
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 257 tgtatgccta tcacattgtt ggacaacatc atagcaggat ggcattcgg aagcagcatg 360
 258 tgcaagatca gtggctgtt gcaaggggata tcagttcggg cttccgtctt caccttggtt 420
 259 gcaatagctg tggacagatt ccgtctgtgt gtcataccct ttaagccaaa gctcactgtc 480
 260 aagacagcct ttgtcacatg tttttttttt tttttttttt ccatcgccat tatgactcca 540
 261 tctgcaataa ttgttacatgtt acaagaagaa aaataactacc ttgttgatgtt cagctccac 600
 262 aataaaaacca gcacagtcta ctgggtgtgg gaggactggc caagacacga aatgaggagg 660
 263 atctataccca cgggtgttattt tgccatcatc tatcttgc tctctctact cattttttatc 720
 264 atgtatgcaa ggattggggc ttccctcttc aagacggcag cacactgcac aggcaaggcag 780
 265 cgtccagtgc agtgcgtatg tcaagagaaa cagaaggta tcaagatgtt gctgactgtg 840
 266 gccccttcc tcatccttcc ctggcttccc ctgtggaccc tttttttttt ctcagactat 900

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267 actgacctgt ctccctaacaa actgcgtatc atcaacatct acatctaccc tttcgcccac 960
268 tggctcgccct tctgcaacag cagtgtcaac cctattattt atggattttt taatgaaaat 1020
269 tttcgcaatg gtttccaaga tgctttccag atctgccaaa agaaagccaa gccccaggaa 1080
270 gcctattccc tgagagcgaa acgcaacata gtcataaaaca catcgccct gctgggtcag 1140
271 gaaccggtgtt ctcaaaaccc aggtggggaa aatttggat gtggaaaaag tgcagacaat 1200
272 ccacacagga atccttgata gaggaatg 1228

VERIFICATION SUMMARY

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L:0 M:201 W: Mandatory field data missing, FILE REFERENCE

L:8 M:270 C: Current Application Number differs, Replaced Current Application Number

L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:28 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1

L:33 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1